

```

1 gcgtctccac cccctcagcgg gcggcggtga gtgcgccagg ccagcgccgg cgtgggaccg
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121 gagtttagagt acccttccaa AATGGCTGCT ATTAAGGAAG AGAGAGAGGT GGAAGATTAC
181 AAGAGAAAAA GGAAGACGAT CAGCACAGGC CATGAGCCTA AGGAGCCAGA GCAGTTGAGA
241 AAGCTGTTCA TTGGAGGTCT GAGCTTCGAG ACGACGGATG ATAGCTTGAG AGAGCACTTT
301 GAAAAATGGG GCACACTCAC GGACTGTGTG GTGATGAGAG ACCCACAAAC AAAACGTTCC
361 AGAGGCTTGG GCTTTGTTAC TTACTCTTGC GTGGAAGAGG TGGATGCGGC CATGAGCGCT
421 CGACCCACATA AGGTGGATGG ACGTGTGGTT GAACCAAGA GAGCAGTTTC AAGGGAGGAT
481 TCTGTAAAGC CTGGGGCGCA TCTCACAGTA AAAAAATAT TTGTTGGTGG CATTAAAGAA
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601 GAAGTCATGG AAGACAGACA AAGTGGAAAG AAAAGAGGCT TCGCTTTTGT AACTTTTGAT
661 GATCAGCATA CAGTTGATAA AATTGTTGTT CAGAAATACC ATACTATAAA TGGTCATAAC
721 TGCCAAGATA AAAAAGCACT CTCAAAACAA GAGATGCAGA CTGCCAGCTC TCAGAGAGGT
781 CGTGGGGGTG GTTCAGGCAA CTTTCATGCT CGTGGAAAT TTGAGGTTGG TGGAGGAAC
841 TTTGGCCGAG GAGGAAACTT TGGTGAAGA GGAGGCTATG GGGGTGGTGG TGGCGGTGGT
901 GGGAGCAGAG GAAGCTTTGG GGGTGGTGGT GGATACAACG GATTGTTGTA TGGTGGCAAC
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1021 TATGGAACC CAGGTGGTGG ATATGGAGGT GGAGGAGGAG GATATGGTGG CTACATGAA
1081 GGAGGCAATT TTGGAGGTGG TAATTATGGA GGCAGTGGAA ACTACAATGA CTTTGGTAA
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1501 gctatttggtt aatgcaatgt agtgcgttta gatgtacatc ctgaggtctt tatctgtgt
1561 agctttgtct tccttttttc tttttatttt cccattacat caggtatatt gccctgtaaa
1621 ttgtggtagt ggtaccagga ataaacaaat taaggaattt ttggcttttc aaaaaaaaaa
1681 aaaaaaaaaa

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Fig. 1a

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CHKA1 - MAAIKEEREVEDYKRKRKTISTGHEPKEPEQLRKLFIGGLSFETTDLSLR -50
HUMA1 - M-----SKSESPKEPEQLRKLFIGGLSFETTDLSLR -31

CHKA1 - EQFEKWTGLTDCVVMRDPQTKRSRGFGFVTYSCVEEVDAAARSAPHKVDG -100
HUMA1 - SHFEQWGLTDCVVMRDPNPKRSRGFGFVTYATVEEVDAAARNAPHKVDG -81

CHKA1 - RVVEPKRAVSREDSVKPGAHLTVKKIFVGGIKEDTEEYNLRGYFETYGKI -150
HUMA1 - RVVEPKRAVSREDSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYGKI -131

CHKA1 - ETIEVMEDRQSGKKRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEDKKAL -200
HUMA1 - EVIEIMDRGSGKKRGFAFVTFDDHDSVDKIVIQKYHTVNGHNCVVRKAL -181

CHKA1 - SKQEMQTASS-QRGRGGSGNFMGRGNFGGGG-----NFGRGGNFEGG -242
HUMA1 - SKQEMASASSQGRSGS-----GNFGGRGGGFGGNDNFGRGGNFSG -224

CHKA1 - RGGYGGGGGGGSRGSFGGGDCYNGFDDGNYGGGPGYGSRGYGGGGGP -292
HUMA1 - RGGFSGSRGGGGYGS---GDGYNGFGNDGS----- -252

CHKA1 - GYGNPGGGYGGGGGGYGGYNEGNGFGGGNYGGSGNYNDFGNYSCQQQSNY -342
HUMA1 - -----NFGGGGSYNDFGNYNNQS-SNF -273

CHKA1 - GPMKGGSGFGRSSGSPYGGG-----YGSAGSGGGY-GRRF -378
HUMA1 - GPMKGG-NFGGRSSG-PYGGGGQYFAKPRNQGGYGGSSSSSYGSGRRF -320

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Fig. 1b

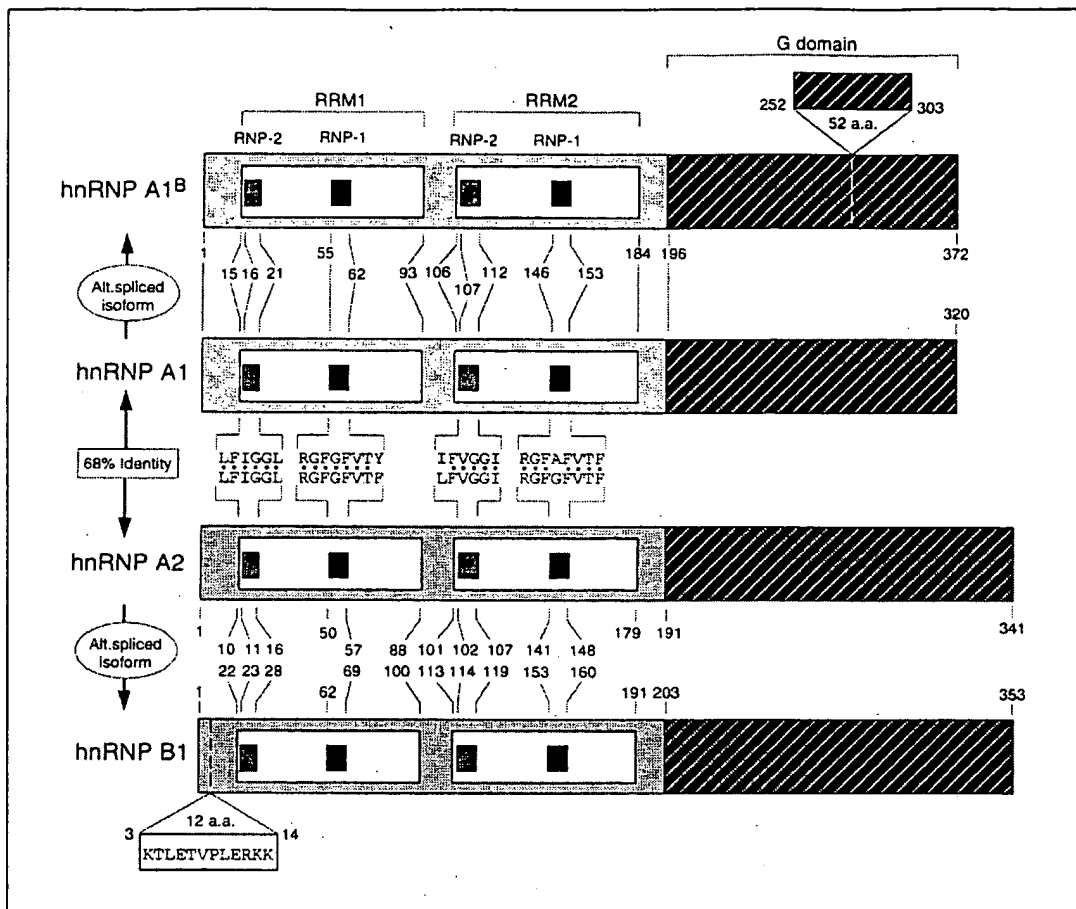


Fig. 2

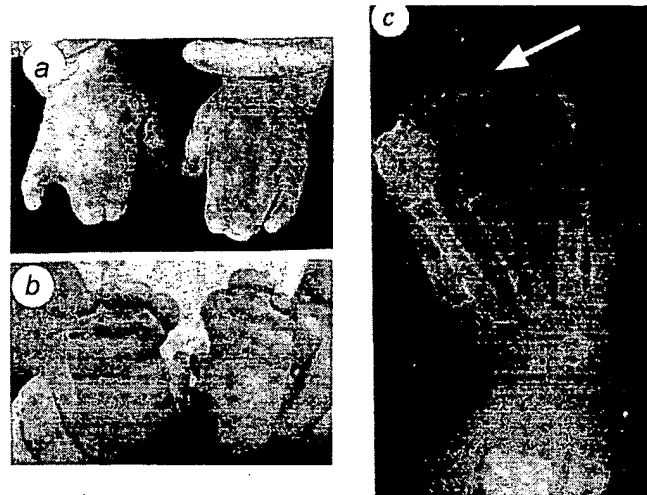


Fig. 3

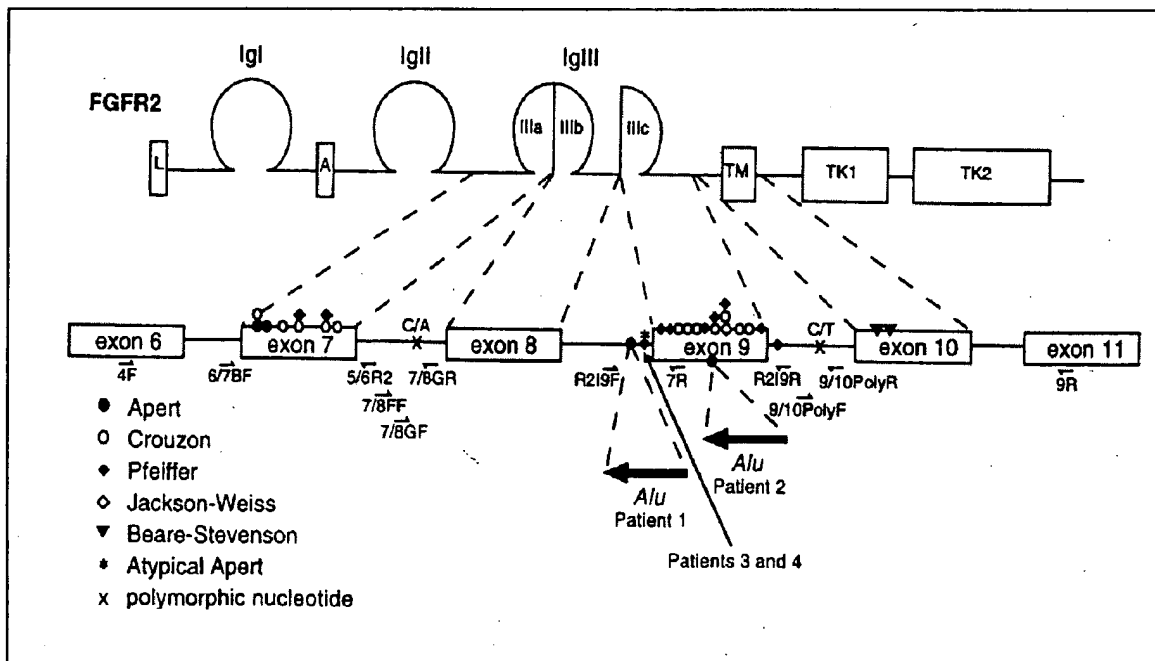
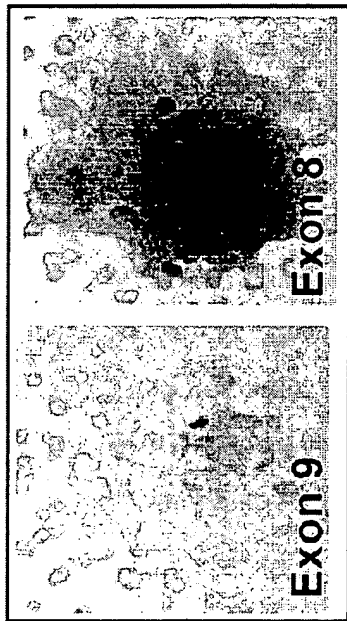
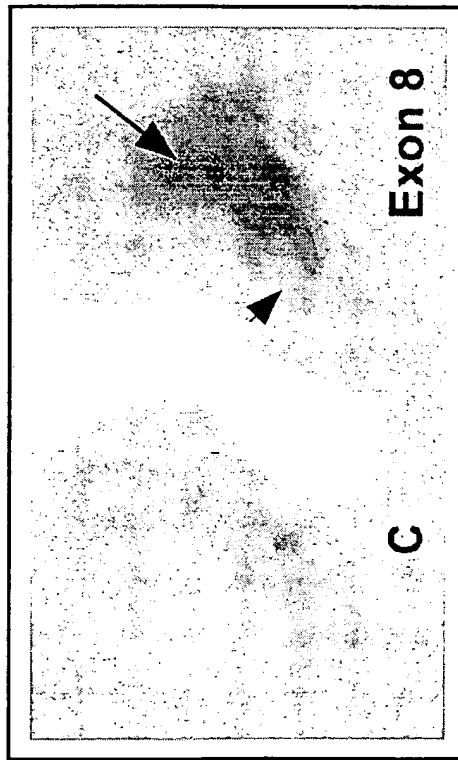


Fig. 4

A.



B.



C.

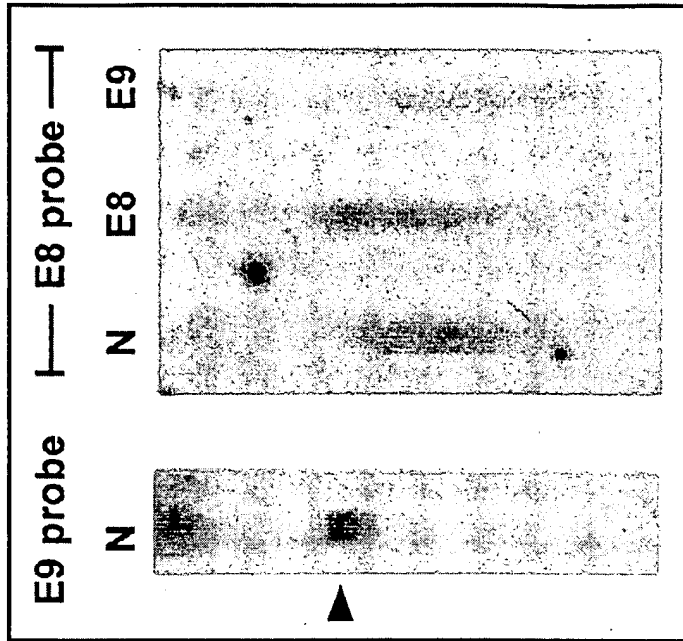


Fig. 5